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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2011; month=1; day=21; hr=9; min=7; sec=0; ms=643;]

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Application No: 10528183

Version No: 2.0

Input Set:

Output Set:

Started: 2011-01-11 14:42:59.791

Finished: 2011-01-11 14:43:04.929

Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 138 ms

Total Warnings: 106

Total Errors: 0

No. of SeqIDs Defined: 106

Actual SeqID Count: 106

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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Input Set:

Output Set:

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Total Warnings: 106
Total Errors: 0
No. of SeqIDs Defined: 106
Actual SeqID Count: 106

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Ullman, Katharine
Liu, Jin
Prunuske, Amy
Dimaano, Christian

<120> METHODS OF INHIBITING CELL CYCLE OF A CELL COMPRISING ADMINISTERING
A NUP153 INHIBITOR

<130> 21101.0045U2

<140> 10528183
<141> 2005-05-27

<150> PCT/US2003/29267
<151> 2003-09-17

<150> 60/411248
<151> 2002-09-17

<160> 106

<170> PatentIn version 3.5

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct

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<211> 1475

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

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Arg Gln Gln His Gln Gly Ile Leu Ser Arg Val Thr Glu Ser Val Lys
35 40 45

Asn Ile Val Pro Gly Trp Leu Gln Arg Tyr Phe Asn Lys Asn Glu Asp
50 55 60

Val Cys Ser Cys Ser Thr Asp Thr Ser Glu Val Pro Arg Trp Pro Glu
65 70 75 80

Asn Lys Glu Asp His Leu Val Tyr Ala Asp Glu Glu Ser Ser Asn Ile
85 90 95

Thr Asp Gly Arg Ile Thr Pro Glu Pro Ala Val Ser Asn Thr Glu Glu
100 105 110

Pro Ser Thr Thr Ser Thr Ala Ser Asn Tyr Pro Asp Val Leu Thr Arg
115 120 125

Pro Ser Leu His Arg Ser His Leu Asn Phe Ser Met Leu Glu Ser Pro
130 135 140

Ala Leu His Cys Gln Pro Ser Thr Ser Ser Ala Phe Pro Ile Gly Ser
145 150 155 160

Ser Gly Phe Ser Leu Val Lys Glu Ile Lys Asp Ser Thr Ser Gln His
165 170 175

Asp Asp Asp Asn Ile Ser Thr Thr Ser Gly Phe Ser Ser Arg Ala Ser
180 185 190

Asp Lys Asp Ile Thr Val Ser Lys Asn Thr Ser Leu Pro Pro Leu Trp

195

200

205

Ser Pro Glu Ala Glu Arg Ser His Ser Leu Ser Gln His Thr Ala Thr
210 215 220

Ser Ser Lys Lys Pro Ala Phe Asn Leu Ser Ala Phe Gly Thr Leu Ser
225 230 235 240

Pro Ser Leu Gly Asn Ser Ser Ile Leu Lys Thr Ser Gln Leu Gly Asp
245 250 255

Ser Pro Phe Tyr Pro Gly Lys Thr Thr Tyr Gly Gly Ala Ala Ala Ala
260 265 270

Val Arg Gln Ser Lys Leu Arg Asn Thr Pro Tyr Gln Ala Pro Val Arg
275 280 285

Arg Gln Met Lys Ala Lys Gln Leu Ser Ala Gln Ser Tyr Gly Val Thr
290 295 300

Ser Ser Thr Ala Arg Arg Ile Leu Gln Ser Leu Glu Lys Met Ser Ser
305 310 315 320

Pro Leu Ala Asp Ala Lys Arg Ile Pro Ser Ile Val Ser Ser Pro Leu
325 330 335

Asn Ser Pro Leu Asp Arg Ser Gly Ile Asp Ile Thr Asp Phe Gln Ala
340 345 350

Lys Arg Glu Lys Val Asp Ser Gln Tyr Pro Pro Val Gln Arg Leu Met
355 360 365

Thr Pro Lys Pro Val Ser Ile Ala Thr Asn Arg Ser Val Tyr Phe Lys
370 375 380

Pro Ser Leu Thr Pro Ser Gly Glu Phe Arg Lys Thr Asn Gln Arg Ile
385 390 395 400

Asp Asn Lys Cys Ser Thr Gly Tyr Glu Lys Asn Met Thr Pro Gly Gln
405 410 415

Asn Arg Glu Gln Arg Glu Ser Gly Phe Ser Tyr Pro Asn Phe Ser Leu
420 425 430

Pro Ala Ala Asn Gly Leu Ser Ser Gly Val Gly Gly Gly Gly Gly Lys
435 440 445

Met Arg Arg Glu Arg Thr Arg Phe Val Ala Ser Lys Pro Leu Glu Glu
450 455 460

Glu Glu Met Glu Val Pro Val Leu Pro Lys Ile Ser Leu Pro Ile Thr
465 470 475 480

Ser Ser Ser Leu Pro Thr Phe Asn Phe Ser Ser Pro Glu Ile Thr Thr
485 490 495

Ser Ser Pro Ser Pro Ile Asn Ser Ser Gln Ala Leu Thr Asn Lys Val
500 505 510

Gln Met Thr Ser Pro Ser Ser Thr Gly Ser Pro Met Phe Lys Phe Ser
515 520 525

Ser Pro Ile Val Lys Ser Thr Glu Ala Asn Val Leu Pro Pro Ser Ser
530 535 540

Ile Gly Phe Thr Phe Ser Val Pro Val Ala Lys Thr Ala Glu Leu Ser
545 550 555 560

Gly Ser Ser Ser Thr Leu Glu Pro Ile Ile Ser Ser Ser Ala His His
565 570 575

Val Thr Thr Val Asn Ser Thr Asn Cys Lys Lys Thr Pro Pro Glu Asp
580 585 590

Cys Glu Gly Pro Phe Arg Pro Ala Glu Ile Leu Lys Glu Gly Ser Val
595 600 605

Leu Asp Ile Leu Lys Ser Pro Gly Phe Ala Ser Pro Lys Ile Asp Ser
610 615 620

Val Ala Ala Gln Pro Thr Ala Thr Ser Pro Val Val Tyr Thr Arg Pro
625 630 635 640

Ala Ile Ser Ser Phe Ser Ser Ser Gly Ile Gly Phe Gly Glu Ser Leu
645 650 655

Lys Ala Gly Ser Ser Trp Gln Cys Asp Thr Cys Leu Leu Gln Asn Lys
 660 665 670

Val Thr Asp Asn Lys Cys Ile Ala Cys Gln Ala Ala Lys Leu Ser Pro
 675 680 685

Arg Asp Thr Ala Lys Gln Thr Gly Ile Glu Thr Pro Asn Lys Ser Gly
 690 695 700

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 725 730 735

Pro Glu Ala Ile Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr
 740 745 750

Cys Val Lys Arg Ala Leu Thr Leu Thr Val Val Ser Glu Ser Ala Glu
 755 760 765

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 770 775 780

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 835 840 845

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Lys Ala Asp Ser Thr Lys Cys Leu Ala Cys Glu Ser Ala Lys Pro Gly
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Thr Lys Ser Gly Phe Lys Gly Phe Asp Thr Ser Ser Ser Ser Ser Asn
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Ser Ala Ala Ser Ser Ser Phe Lys Phe Gly Val Ser Ser Ser Ser Ser
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Gly Pro Ser Gln Thr Leu Thr Ser Thr Gly Asn Phe Lys Phe Gly Asp
915 920 925

Gln Gly Gly Phe Lys Ile Gly Val Ser Ser Asp Ser Gly Ser Ile Asn
930 935 940

Pro Met Ser Glu Gly Phe Lys Phe Ser Lys Pro Ile Gly Asp Phe Lys
945 950 955 960

Phe Gly Val Ser Ser Glu Ser Lys Pro Glu Glu Val Lys Lys Asp Ser
965 970 975

Lys Asn Asp Asn Phe Lys Phe Gly Leu Ser Ser Gly Leu Ser Asn Pro
980 985 990

Val Ser Leu Thr Pro Phe Gln Phe Gly Val Ser Asn Leu Gly Gln Glu
995 1000 1005

Glu Lys Lys Glu Glu Leu Pro Lys Ser Ser Ser Ala Gly Phe Ser
1010 1015 1020

Phe Gly Thr Gly Val Ile Asn Ser Thr Pro Ala Pro Ala Asn Thr
1025 1030 1035

Ile Val Thr Ser Glu Asn Lys Ser Ser Phe Asn Leu Gly Thr Ile
1040 1045 1050

Glu Thr Lys Ser Ala Ser Val Ala Pro Phe Thr Cys Lys Thr Ser
1055 1060 1065

Glu Ala Lys Lys Glu Glu Met Pro Ala Thr Lys Gly Gly Phe Ser
1070 1075 1080

Phe Gly Asn Val Glu Pro Ala Ser Leu Pro Ser Ala Ser Val Phe
1085 1090 1095

Val Leu Gly Arg Thr Glu Glu Lys Gln Gln Glu Pro Val Thr Ser

1100

1105

1110

Thr Ser Leu Val Phe Gly Lys Lys Ala Asp Asn Glu Glu Pro Lys
1115 1120 1125

Cys Gln Pro Val Phe Ser Phe Gly Asn Se